

Sequence Comparison A

RESULT 13

AAX26588

ID AAX26588 standard; DNA; 2169 BP.

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AC AAX26588;

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DT 16-JUN-1999 (first entry)

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DE Nucleotide sequence of murine KCNQ2 (formerly known as (KvLR1)).

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KW KCNQ protein; nervous system-specific potassium channel;

KW neuronal excitability; neurotransmitter release; KCNQ modulator;

KW ataxia; myokymia; seizure; Alzheimer's disease; Parkinson's disease;

KW age-associated memory loss; learning deficiency; motor neuron disease;

KW epilepsy; stroke; ss.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT CDS 1..2169

FT /*tag= a

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PN WO9907832-A1.

XX

PD 18-FEB-1999.

XX

PF 26-JUN-1998; 98WO-US13276.

XX

PR 12-AUG-1997; 97US-0055599.

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PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PI Blanar MA, Dworetzky S, Gribkoff VK, Levesque PC;

PI Little WA, Neubauer MG, Yang W;

XX

DR WPI; 1999-190047/16.

DR P-PSDB; AAY01530.

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PT New potassium channels, KCNQ2 and KCNQ3 - may be involved in

PT neurotransmission and neuroprotection, used to treat, e.g. ataxia

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PS Claim 7; Fig 10A-D; 64pp; English.

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CC The present sequence encodes murine KCNQ2/KvLR1. KCNQ proteins are

CC nervous system-specific potassium channels. In neurons, potassium

CC channels regulate neuronal excitability, action potential shape

CC and firing pattern, and neurotransmitter release. KCNQ modulators

CC may be used to treat disorders such as ataxia, myokymia, seizures,

CC Alzheimer's disease, Parkinson's disease, age-associated memory

CC loss, learning deficiencies, motor neuron diseases, epilepsy, and

CC stroke.

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SQ Sequence 2169 BP; 466 A; 622 C; 635 G; 446 T; 0 other;

Query Match 18.9%; Score 510; DB 20; Length 2169;

Best Local Similarity 58.1%; Pred. No. 1e-139;

Matches 1043; Conservative 0; Mismatches 670; Indels 81; Gaps 5;

QY 64 GGCCTGCTACTGCTGGGCACCCGCGCGCCACGCTTGGTGGCGGCGGCGGTGGCCTGAGG 123

Db 67 GGCTTCGTGGGGCTGGACCCGCGCGCCGACTCCACACGCGACGGCGGCTACTCATC 126

QY 124 GAGAGCCGCCGGGGCAAGCAGGGGCCCGGATGAGCCTGCTGGGAAGCCGCTCTTTAC 183

Db 127 GCGGGCTCCGAGGCCCAAGCGCGGCAGCGTTTGTAGCAAGCCGCGACGGCGGCGCG 186

QY 184 ACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACGGCGGGTGCAGAACTACCTGTAC 243

Db	187	GGAGCCGGGAAGCCCCGAAGCGCAACGCCTTCTACCGCAAGCTGCAGAATTTCTCTAC	246
Qy	244	AACGTGCTGGAGAGACCCCGCGGCTGGGCGTTTCATCTACCACGCTTCGTTTTTCTCCTT	303
Db	247	AACGTGCTAGAGCGGCCCGCGGCTGGGCGTTTCATCTACCACGCTACGTGTTCTCTTTTA	306
Qy	304	GTCTTTGGTTGCTTGATTTTGTCTAGTGTCTTCTACCATCCCTGAGCACACAAAATTGGCC	363
Db	307	GTCTTCTCCTGCCTTGTGCTTCTGTGTTTTCCACCATCAAGGAGTACGAGAAGAGCTCT	366
Qy	364	TCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCCTTGGTTTGGAGTTCATC	423
Db	367	GAGGGGGCCCTCTACATCTTGGAAATCGTGACTATCGTGGTATTCGGTGTTGAGTACTTT	426
Qy	424	ATTGCAATCTGGTCTGCGGTTGTCTGTTGTCGATATAGAGGATGGCAAGGAAGACTGAGG	483
Db	427	GTGAGGATCTGGGCTGCAGGCTGCTGTTGCCGGTATCGAGGCTGGAGGGGCAGGCTCAAG	486
Qy	484	TTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTGTTCTTATCGTTCAATAGCAGTT	543
Db	487	TTTGCCAGGAAGCCGTTCTGTGTGATTGATATCATGGTGTGATTGCCTCCATTGCTGTG	546
Qy	544	GTTTTCTGCAAAAACCTCAGGGTAATATTTTTTGCCACGTCTGCACCTCAGAAGTCTCCGTTTC	603
Db	547	CTGGCTGCTGGTTCACAGGGCAATGTCTTTTGCCACATCTGCGCTTCGGAGCTTGGCGTTC	606
Qy	604	CTACAGATCCTCCGCATGGTGGCGCATGGACCGAAGGGGAGGCACTTGGAAATTACTGGGT	663
Db	607	TTGCAAACTCTGCGGATGATCCGTATGGACCGGAGGGGTGGCACTTGGAAAGCTCTTGGGA	666
Qy	664	TCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTGGTT	723
Db	667	TCGGTAGTCTACGCTCACAGCAAGGAGCTGGTGACTGCCTGGTACATTGGCTTCTCTGTC	726
Qy	724	CTTATTTTTTCGTCCTTCTGTCTATCTGGTGGAAAAGGATGCCAATAAAGAGTTTTCT	783
Db	727	CTCATCCTGGCCTCATTCTGGTGTACTTGGCAGAAAAGGGTGAGAATGACCACTTTGAC	786
Qy	784	ACATATGCAGATGCTCTCTGGTGGGGCACAATTACATTGACAACTATTGGCTATGGAGAC	843
Db	787	ACCTACGCAGATGCACTCTGGTGGGGTCTGATCACCTGACGACCATTGGCTACGGGGAC	846
Qy	844	AAAACTCCTTAACCTGGCTGGGAAGATTGCTTTCTGCAGGCTTGCACCTCCTTGGCATT	903
Db	847	AAGTACCCTCAGACCTGGAACGGGAGGCTGCTGGCAGCGACCTTACCCTCATTGGTGTC	906
Qy	904	TCTTTCTTTGCACTTCTCTGCCGGCATTCTTGGCTCAGGTTTTGCAATTAAGTACAAGAA	963
Db	907	TCGTTCTTTGCTCTTCTGCTGGCATTTTGGGATCCGGCTTTGCCCTGAAAGTCCAAGAG	966
Qy	964	CAACACCGCCAGAAACACTTTGAGAAAAAGGAACCCAGCTGCCAACCTCATTAGTGT	1023
Db	967	CAGCATCGGCAGAAACACTTTGAGAAACGGCGGAACCTGCGGCAGGTCTGATCCAGTCT	1026
Qy	1024	GTTTGGCGTAGTTACGCAGCTGATGAGAAAT-----	1054
Db	1027	GCCTGGAGATTCTATGCTACTAACCTCTCACGCACCGACCTGCACTCCACGTGGCAGTAC	1086
Qy	1055	-----CTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGAC	1098
Db	1087	TACGAGCGGACAGTCACTGTCCCATGTACAGACTCATCCACCTCTGAACCACTGGAG	1146
Qy	1099	ACCTGCAGCCCTACCAAGA-----AAGAACAAGGGGAA	1131
Db	1147	CTGCTGAGGAATCTCAAGAGCAAACTCTGGACTCACCTTCAGGAAGGAGCCACAGCCAGAG	1206
Qy	1132	GCATCAAGCAGTCAGAAGCTAAGTTTTAAGGAGCGAG---TGCGCATGGCTAGCCCCAGG	1188
Db	1207	CCATACCAAGTCAAGAGTTCAGTTTGAAGATCGTGTCTTCTCCAGCCCCGAGGCATG	1266
Qy	1189	GGCCAGAGTATTAAGAGCCGACAAGCCTCAGTAGGTGACAGGAGTCCCAAGCACCGAC	1244

Db 1267 GCTGCCAAGGGAAAGGGTCTCCCCAGGCCAGACGGTCCGGCGGTCCCCAGTGCGGAT 1326
 Qy 1249 ATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACC 1308
 Db 1327 CAGAGTCTTGATGACAGCCCGAGCAAGGTGCCCAAGAGCTGGAGCTTTGGTGACCGCAGC 1386
 Qy 1309 CGCTTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAGTGATAGATGCTGAC 1368
 Db 1387 CGCACACGCCAGGCTTCCGCATCAAGGGTGCTGCATCCCGGCAGAATTGAGAAGCAAGC 1446
 Qy 1369 ACAGCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTG 1428
 Db 1447 C---TCCCTGGGGAGGACATCGTAGAGGACAACAAGAGCTGTAAGTGCAGTTTGTGACT 1503
 Qy 1429 GAAGACCTCACCCACCACCTAAAGTGTGATTCGAGCTATCAGAATTATGAAATTCAT 1488
 Db 1504 GAAGATCTTACCCCTGGCCTCAAAGTTAGCATCAGAGCTGTGTGTGTATGCGGTTCTTG 1563
 Qy 1489 GTTGCAAAACGGAAGTTTAAGGAAACGTTACGTCCATATGATGTAAAAGATGTCATTGAA 1548
 Db 1564 GTATCTAAGCGAAAGTTCAAAGAGAGTCTGCGCCCATATGATGTGATGGACGTCATCGAA 1623
 Qy 1549 CAATATCTGTGTCATCTGGACATGTTGTGTAGAATTAAAAGCCTTAAACACGTGTT 1608
 Db 1624 CAGTACTCGGCTGGACACTTGGATATGTTGTCCCGCATCAAGAGCCTGCAGTCCAGAGTG 1683
 Qy 1609 GATCAAATTCTTGAAAAGGGCAAATCACATCAGATAAGAAGAGCCGAGAGAAAATAACA 1668
 Db 1684 GACCAGATTGTGGGGCGGGGCCCAACAATAACGATAAGGA---TCGCACCAAAGGCCCA 1740
 Qy 1669 GCAGAACATGAGACCACAGACGATCTCAGTATGCTCGGTGCGGTGGTCAAGGTTGAAAAA 1728
 Db 1741 GCGGAAACGGAGCTGCCGAAGACCCAGCATGATGGACGGCTTGGGAAGGTGGAGAAA 1800
 Qy 1729 CAGGTACAGTCCATAGAGTCCAAGCTGGACTGCCTACTAGACATCTATCAACAG 1782
 Db 1801 CAGGTCTGTCCATGGAAGAAGCTCGACTTCTTGGTGAGCATCTATACACAG 1854